

PD - 12/3/98, FD - 9/28/1999

177

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2002, 13:48:36 ; Search time 1341.91 Seconds
(without alignments)
1954.715 Million cell updates/sec

Title: US-09-407-804A-8
Perfect score: 159
Sequence: 1 atggttaaccaagaattttt.....cgcgtatcgctgaattataa 159

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues
Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_on.*
- 20: em_or.*
- 21: em_ov.*
- 22: em_pat.*
- 23: em_ph.*
- 24: em_pl.*
- 25: em_ro.*
- 26: em_sts.*
- 27: em_sy.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_htgo_hum.*
- 31: em_htgo_inv.*
- 32: em_htgo_rod.*
- 33: em_htg_hum.*
- 34: em_htg_inv.*
- 35: em_htg_rod.*
- 36: em_htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149.4	94.0	42942	7	AB045978 Staphyloc
2	143	89.9	348527	1	AP003360 Staphyloc
3	52.6	33.1	43081	7	AF001553 Bacterioph
4	40	25.2	45636	7	AB044554 Staphyloc
5	36.8	23.1	4620	9	AB037782 Homo sapi
6	36.8	23.1	25943	3	CEC3866 Caenorhabdi
7	36.8	23.1	161198	2	AC015867 Homo sapi
8	36.8	23.1	175271	2	AC090898 Homo sapi
9	36.8	23.1	188346	2	AC010189 Homo sapi
10	36.8	23.1	189009	2	AC068588 Homo sapi
11	35.8	22.5	149109	2	AC023181 Homo sapi
12	35.8	22.5	149246	9	AC066580 Homo sapi
13	35.8	22.5	207600	9	AC024910 Homo sapi
14	35.8	22.5	222542	9	AC022379 Homo sapi
15	35.6	22.4	105222	8	AC006220 Arabidops
16	35.2	22.1	171200	9	AC090946 Homo sapi
17	35.2	22.1	171543	33	AC019245 Homo sapi
18	35.2	22.1	179717	9	AC087858 Homo sapi
19	34.8	21.9	166065	2	AC013552 Homo sapi
20	34.8	21.9	171698	2	AL359175 Homo sapi
21	34.8	21.9	173852	2	AL158160 Homo sapi
22	34.4	21.6	153988	2	AC091530 Papio cyn
23	34.4	21.6	200964	2	AC091658 Papio cyn
24	33.6	21.1	87235	2	AC022963 Homo sapi
25	33.6	21.1	134841	9	AC016689 Homo sapi
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39	32.8	20.6	162714	2	AC027569 Homo sapi
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ALIGNMENTS

RESULT 1

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DEFINITION	Staphylococcus aureus temperate phage phiSLT genomic DNA, complete sequence.				
ACCESSION	AB045978				
VERSION	AB045978.1	GI:12697822			
KEYWORDS					
SOURCE	Staphylococcus aureus temperate phage phiSLT DNA.				
ORGANISM	Staphylococcus aureus temperate phage phiSLT Viruses.				
REFERENCE	1 (sites)				
AUTHORS	Narita,S., Kaneko,J., Chiba,J., Piemont,Y., Jarraud,S., Etienne,J. and Kamio,Y.				
TITLE	Phage conversion of Pantone-Valentine leukocidin in Staphylococcus aureus: molecular analysis of a PVL-converting phage, phiSLT				
JOURNAL	Gene 268 (1-2), 195-206 (2001)				
MEDLINE	21261956				
REFERENCE	2 (bases 1 to 42942)				
AUTHORS	Kaneko,J., Narita,S. and Kamio,Y.				

```

TITLE
JOURNAL
Direct Submission
Submitted (12-JUN-2000) Jun Kaneko, Tohoku University, Graduate
School of Agricultural Science; 1-1 Tsutsumidori Amamiyamachi,
Sendai, Miyagi 981-8555, Japan
(E-mail: jkaneko@biochem.tohoku.ac.jp, Tel:81-22-717-8781,
Fax:81-22-747-8780)
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Matches 153; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 11898 ATGCTAACCAAGAATTTTTCGAAATTTAAACTTTGAGTGTTCAGATATGTCAGCTCAGAAA 11957
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QY 61 ctcatagatgagcacaggcgatgaaataggttgatgcagacctattatccaaaaactt 120
DB 11958 CTCTATACGAGGCACAGGCGGATGAAATTAAGTTATGACCTATTATTCACAAAACCTT 12017
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QY 121 gcagaaagctatcacagcccgctatcgtcgaaatttaa 159
DB 12018 GCAGAACGTATACACGCCCGCTATGTCGTAATTTAA 12056
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RESULT 2
AP003360
LOCUS
DEFINITION
Staphylococcus aureus subsp. aureus Mu50 genomic DNA, complete
sequence, section 3/9.
ACCESSION
AP003360 BA000017
VERSION
AP003360.2 GI:14246388
KEYWORDS
SOURCE
Staphylococcus aureus subsp. aureus Mu50 (sub_species:aureus Mu50,
strain:Mu50) DNA.
ORGANISM
Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
1 (sites)
REFERENCE
AUTHORS
Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I.,
Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M.,
Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
Mizutani-Ui,Y., Kobayashi,N., Tanaka,T., Sawano,T., Inoue,R.,
Kaito,C., Sekimizu,K., Hiramawa,H., Kuhara,S., Goto,S.,

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TITLE	JOURNAL	MEDLINE	REFERENCE	AUTHORS	TITLE	JOURNAL
Yabuzaki, J., Kanehisa, M., Yamashita, A., Oshima, K., Furuya, K., Yoshino, C., Shiba, T., Hattori, M., Ogasawara, N., Hayashi, H. and Hiramatsu, K.	Lancet 357 (9264), 1225-1240 (2001)	21311952	2 (bases 1 to 348527)	Ohta, T.	Direct Submission	Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College of Medical Technology and Nursing, Department of Medical Technology, 1-1-1 Ten-noodai, Tsukuba, Ibaraki 305-8577, Japan (E-mail: tohta@tsukuba.ac.jp, Tel: 81-298-53-3454, Fax: 81-298-53-3454)
Whole genome sequencing of methicillin-resistant <i>Staphylococcus aureus</i>						On May 29, 2001 this sequence version replaced gi:13874937.
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REFERENCE 2 (bases 1 to 43081)
AUTHORS Sugai, M., Yamaguchi, T., Hayashi, T., Nakasone, K. and Takami, H.
TITLE Direct Submission
JOURNAL Microbiology: Kasumi 1-2-3, Hiroshima, Faculty of Dentistry, Microbiology: Kasumi 1-2-3, Hiroshima, Faculty of Dentistry, Japan (E-mail: sugai@hiroshima-u.ac.jp, Hiroshima 734-8553, Japan (E-mail: sugai@hiroshima-u.ac.jp, Tel: 81-82-257-5637, Fax: 81-82-257-5639)

FEATURES
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/codon_start=1
/transl_table=11
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/db_xref="GI:8918423"
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VEVIKNIITQQKIMK"
complement(3760. .4242)
/note="ORF9
unknown"
/codon_start=1
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/db_xref="GI:8918424"
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YENNEVELNFVANDSSRTHLEELIFLDKKNKVLTPINVLESSEYSLGIYNPSYL
HAPIDKQDKPEVMIANSSSEFLYKFELEPAFIVSNORINKLKKYKILISTDSVEHN
"
4687. .4872
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unknown"
/codon_start=1
/transl_table=11
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/db_xref="GI:8918425"
/translation="MLNLKELREKGITRYQLAKLTELQNSTIRSIETEVKNPGLTV
KKICDALQVDIANVKEK"
4874. .5626
/note="ORF11
similar to phage phi PVL antirepressor"
/codon_start=1
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/db_xref="GI:8918426"
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FPRMLKYGEENTDYTAIAOKRATAGQNMTHYIDHALTDTAKEIAMTQORSPGKRAR
QYFIOVERKAWNSPEMIMORALKAIANNITNOLETKIERDKPKIVFADAVATTTSILVG
ELAKTIKONGINIGORRLFEWLRONGFLIKRKGVDYNNMPTQYSMERELFEIKETSITH
SDGHTSISKTPKVTGCKGOQYFVNKFLGETQT"
complement(5731. .6396)
/note="ORF12
unknown"
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/db_xref="GI:8918427"
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LEIQTVNNMNSIRINQSKLSDWASYHQVTKNHPMKSNLFSKILDEFISSNSFP
DDEQKVTSTHRLKRSFVDVDPVLGKTVNSAHPIDDVNTKESDKIFYKSIINOYFLAPS
SSFVHDVSLTVAKSVAVNMFVRTANDDYVNYFFSTAVIAVCYVASCANAFDLKKNRKK
DFK"
6467. .6688
/note="ORF13
unknown"
/codon_start=1
/transl_table=11
/protein_id="BAA97599.1"
/db_xref="GI:8918428"
/translation="MIKNSLOAKELAVILSVSKAGQIIRLNLKELEDEGYIAIRGR

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IPVOLARKFPYHDLSDORIMEELKENE"
6681..6842
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similar to phage phi PVL ORF38"
/codon_start=1
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/protein_id="BAA97600.1"
/db_xref="GI:8918429"
/transl_table="MSKTKSYLLAVLCFTVLAIVLMPFLYTTAWSTAGFASITATFI
FYKEYFEE"
6936..7196
/contig="ORF15
similar to phage phi PVL ORF39"
/codon_start=1
/transl_table=11
/protein_id="BAA97601.1"
/db_xref="GI:8918430"
/transl_table="MYEIGEIRKNIHVNGFDKIFILKGMGISTQVKDMNVPK
HAYVDENOLDWASDLFNOAIDEWTEENTDQDRILNLVNRW"
7206..7427
/contig="ORF16
unknown"
/codon_start=1
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/protein_id="BAA97602.1"
/db_xref="GI:8918431"
/transl_table="MNQTVYIIRHRDMPYITNKPPTDNNSDYSYSTNRNRAREFNGM
EASINMDYHKAIRKTVTETIEYEVEHD"
7420..8199
/contig="ORF17
unknown"
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/protein_id="BAA97603.1"
/db_xref="GI:8918432"
/transl_table="MTBQTNQDVIDLTOLGVKDISKONANKYKFAIYKGFQGTGTF
LTKONALVIDINEDGTVTVEDGAVQIKYHFSAVIKMLPKIIEOLRENGKQIDVL
VIETIQLRDITDDINDGSKRPTFNDWGECASTRVSIYRISKLOHYOFHLAIS
Query Match 33.18; Score 52.6; DB 7; Length 43081;
Best Local Similarity 58.7%; Pred. No. 1.9e-05;
Matches 91; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 5 taaccagaagaatttttaaaaaactaaacttgatggttcagatgtagctcgaaactca 64
Db 11922 TCACAAACAAATATAAAGAAATATTACATTGTAGAGATGATATGCTCAAAAGATGA 11981
QY 65 tagatgagggcacagggcgatgaaataagttgtacgacctatttatccaaactgcag 124
Db 11982 TTGATTTTGCNAACGGAGACCAAGAAACTTAAAAAACTTATTGATGATGAAGTGAAG 12041
QY 125 aacgtcatcacgccccgcgtatcgtcgaaatataa 159
Db 12042 AAAAAGAGAAGAACCGCAATCGTCGATATATA 12076
RESULT 4
AB044554
LOCUS
DEFINITION
Staphylococcus aureus prophage phipV83 proviral DNA, complete
ACCESSION
AB044554
VERSION
AB044554.1
KEYWORDS
GI:8918747
SOURCE
Staphylococcus aureus prophage phipV83
specific_host:Staphylococcus aureus (strain:P83,
Staphylococcus aureus prophage phipV83
Viruses.
1 (sites)
Kaneko,J., Kimura,T., Kawakami,Y., Tomita,T. and Kamio,Y.
Panton-valentine leukocidin genes in a phage-like particle isolated
from mitomycin C-treated Staphylococcus aureus V8 (ATCC 49775)
Biosci. Biotechnol. Biochem. 61 (11), 1960-1962 (1997)
MEDLINE
98067870
2 (sites)
Zou,D., Kaneko,J., Narita,S. and Kamio,Y.
Complete nucleotide sequence and molecular characterization of
prophage PV83pro carrying lukM-lukF-pv(p83) gene cluster in
Staphylococcus aureus strain P83
Unpublished (2000)
JOURNAL
REFERENCE
3 (bases 1 to 45636)
AUTHORS
Kaneko,J., Zou,D. and Kamio,Y.
TITLE
Direct Submission
JOURNAL
Submitted (09-JUN-2000) to the DDBJ/EMBL/GenBank databases. Jun
Kaneko, Tohoku University, Graduate school of Agricultural Science;
1-1 Tsutsumi-dori Amamiyamachi, Aoba-ku, Sendai, Miyagi 981-8555,
Japan (E-mail: jkaneko@biochem.tohoku.ac.jp, Tel:81-22-717-8781,
Fax:81-22-717-8780)
FEATURES
Location/Qualifiers
1..45636
/organism="Staphylococcus aureus prophage phipV83"
/proviral
/specific_host="Staphylococcus aureus"
/strain="P83"
/db_xref="taxon:129009"
1..156
/note="attP region of phi 11"
complement(423..1139)
/note="C-terminal portion truncated
orf 1"
/codon_start=1
/transl_table=11
/product="integrase"
/protein_id="BAA97808.1"
/db_xref="GI:8918748"
/transl_table="MFVYKDDNTGKVFYSIRYKDYVGNKKMKRGFKKDKAKLAES
EFTONVYKGSNDQPEYIFFDLKNNENLSARSIEKRTTEYNTHIKERFGNLPICKIT
TQCTAFRNLLNDAGSYARSWAGFKAVINAKKHYKLLYDPTLSVTPIPTRKP
QAKPIREFDEKVEQITNDTSRQLTKLLFYSLRIGELALQWKDYNKIKGEIDVNK
KINLSNRKIEYNLKKALKG"
1252..1866
/note="orf 2"
/codon_start=1
/transl_table=11
/product="phi PVL ORF 30 homologue"
/protein_id="BAA97809.1"
/db_xref="GI:8918749"
/transl_table="MTQFLGALLTGLVGYIPYKYLTMIGLVSEKKNIIINTPVLIFS
LTKTRKFMNLDICISLDRKRLFNNGKPVFIKDFENRIIEGELKTYNSAGSDF
DLLEVERODFKVSDLPSENDEYITIKHTLVLDLQKQIKLDLYLMNEY"
complement(2098..2547)
/note="orf 3"
/codon_start=1
/transl_table=11
/protein_id="BAA97810.1"
/db_xref="GI:8918750"
/transl_table="MESKQYLWRYNDIEKRTNMTNKTIDLMNYVEFPKRYTEAKGL
VAQPTTINSTRRVENGMTVCYILDODDDVIDFIFDRIITVFFPENGTEDEYFCE
ILFNSSDTFTLKRLSNYTKDRSYPMKSKINDVNTGKVVLFRDFK"
complement(2583..2768)
/note="orf 4"
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/db_xref="GI:8918751"
/transl_table="MSSYKEIEHLHINTGGKELTQTEAKAFIDSOEFKDMIREAK
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putative"
/codon_start=1
/transl_table=11
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/protein_id="BAA97812.1"
/db_xref="GI:8918752"
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TITLE
JOURNAL
COMMENT
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (04-MAY-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 30, 2001 this sequence version replaced gi:14010896.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L8841
Center clone name: 659_G_19
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
* 8823: contig of 8823 bp in length
* 8824 8923: gap of 100 bp
* 8924 25814: contig of 16891 bp in length
* 25815 25914: gap of 100 bp
* 25915 63597: contig of 37683 bp in length
* 63598 63697: gap of 100 bp
* 63698 145632: contig of 81935 bp in length
* 145633 145732: gap of 100 bp
* 145733 153460: contig of 7728 bp in length
* 153461 153560: gap of 100 bp
* 153561 175931: contig of 22371 bp in length
* 175932 176031: gap of 100 bp
* 176032 187114: contig of 11083 bp in length
* 187115 187214: gap of 100 bp
* 187215 189009: contig of 1795 bp in length.
* Location/Qualifiers
1. .189009
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17"
/clone="RP11-659G19"
/clone_lib="RPCI-11 Human Male BAC"
BASE COUNT 51947 a 39987 c 40656 g 55623 t 796 others
ORIGIN

Query Match
Best Local Similarity 23.1%; Score 36.8; DB 2; Length 189009;
Matches 65; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 15 atttttaaaactaaactaggttcagatgatgcgtcagaactcatagatgagcc 74
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 36136 ATTAATAAATATGCTGATGTGTGTCATATATATACACACACATATATTATGC 36077
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 75 acagggcgatgaataatagggtgtacgacattattatccaaaactgcagaa 126
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 36076 ATGTGGTGAAGAATGTGGCTAGATAGGGGATTTTCTGACACACTGCAAAA 36025
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RESULT 11
AC023181
LOCUS
DEFINITION
AC023181 Homo sapiens clone RP11-20D20, WORKING DRAFT SEQUENCE, 5 unordered
pieces.
ACCESSION
AC023181
VERSION
AC023181.4 GI:14595905
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

```

```

SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 149109)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-20D20
Unpublished
2 (bases 1 to 149109)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Bida,F.,
Boguslavskiy,L., Boukhalter,B., Brown,A., Burkett,G., Castle,A.,
Choepe,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P.,
Dearellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,
Pierre,N., Pisanl,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (09-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 4, 2001 this sequence version replaced gi:12039539.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L3882
Center clone name: 20_D_20
----- Summary Statistics
Sequencing vector: M13; M77815; 3% of reads
Sequencing vector: Plasmid; n/a; 97% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 147126 bases at least Q40
Consensus quality: 148104 bases at least Q30
Consensus quality: 148478 bases at least Q20
Insert size: 150000; agarose-fp
Insert size: 148709; sum-of-contigs
Quality coverage: 8.9 in Q20 bases; agarose-fp
Quality coverage: 9.0 in Q20 bas.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
* 5226: contig of 5226 bp in length
* 5227 5326: gap of 100 bp
* 5327 17559: contig of 12233 bp in length
* 17560 17659: gap of 100 bp
* 17660 74088: contig of 56429 bp in length
* 74089 74188: gap of 100 bp
* 74189 115843: contig of 41655 bp in length
* 115844 115943: gap of 100 bp
* 115944 149109: contig of 33166 bp in length.
* Location/Qualifiers
1. .149109
/organism="Homo sapiens"

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[illegible]

Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, F., Li, G., Li, J., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Li, W., Li, W., Li, Y., Luo, C., Luo, J., Niu, Y., Qi, Q., Qir, X., Song, L., Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, X., Wang, Y., Wu, D., Wang, L., Wang, R., Wang, X., Yang, X., Yu, B., Zeng, Y., Wu, Q., Xie, F., Xuan, Z., Xue, Y., Yan, C., Zhang, M., Zhang, X., Zhang, G., Zhang, H., Zhang, H., Zhang, L., Zhu, N., Yu, J., Zhang, Y., Zhang, Z., Zhu, B.,

Chromosome 3p genomic sequence
Unpublished

TITLE
JOURNAL

**JOURNAL
REFERENCE
AUTHORS**

AUTHORS
Zhong, M., Zhao, Y., Lin, W., Dong, H., Wan, M., Xu, S., Gu, W., Tu, Y.,
Jia, J., Wu, C., Lu, G., Zhang, C., Zhou, Y., Ren, S., Fu, G., Chen, Z., and
Huang, M.
TITLE
Direct Substitution of the α -Carbon of a Ketone with a β -Carbon of an Alkyl Halide

TITLE
JOURNAL

submitted (02-MAR-2000) Genomic Dept., Chinese National Human Genome Center at Shanghai, 315 Guo Shou Jing Road, Shanghai, Shanghai 201203, P. R. China
3 (bases 1 to 207600)
Ding Y

AUTHORS

Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, F., Li, G., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Li, W., Li, Y., Luo, C., Luo, J., Niu, Y., Qi, Q., Song, L., Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, J., Wang, J., Wang, J., Wang, L., Wang, L., Wang, R., Wang, H., Wang, X., Wang, Y., Wu, D., Wu, Q., Xie, F., Xuan, Z., Xue, Y., Yan, C., Zhang, M., Yu, B., Zeng, Y., Zhang, G., Zhang, H., Zhang, L., Zhu, N., Yu, J., and Yang, H.

Direct, S., Yu, J., and Yang, H.

TITLE

TITLE
JOURNAL

COMMENT

COMMENT

On May 28, 2001 this sequence version replaced gi:10305049.

Center: NCBI - Genome Center

http://www.genomics.org.cn
Contact: hgc@igtp.ac.cn

```

Center clone name: 380A22
----- Summary Statistics
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator: ET 5% of reads
Chemistry: Dye-terminator: Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 209300 bases at least Q40
Consensus quality: 211142 bases at least Q30
Consensus quality: 211035 bases at least Q20
Insert size: 207600; sum-of-contigs
Quality coverage:

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FEATURES

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source
Location/Qualifiers
1. 207600
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p"
53351 a 50093 c 50465 g 53691 t
BASE COUNT
ORIGIN

```

Query Match

QY 72 ggcacaggcgatgaaataggttgtagcactattatccaaaaccttgcagaagctca 131
||||| ||||| | | | | | | | | | | | | | | | |
Best Local Similarity 63.2%; Score 35.8; DB 9; Length 207600;
Matches 55; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

72 ggca

59ctgacgacctattatccaaaacttgcagaacgtca 131

1

Db	27140	GACAGGAGGCAATAAAAAATCATTTGTTGTGCAAAAGTGTCCAAAAGTTCCAGAAGGCTA	27081
Qy	132	tacacgccccgcctatcgctgaatatta	158
Db	27080	TACATGCCCCAGGCTTTAGGGACAATTA	27054
RESULT 14			
AC022379/c			
LOCUS			
DEFINITION	AC022379	222542 bp	DNA
ACCESSION	AC022379		
VERSION	AC022379.2		
KEYWORDS	HGC		
			28-MAY-2001
			3p, complete sequence.

RESULT 14
AC022379/C

LOCUS	AC022379	222542 bp	DNA	PRI	28-MAY-2001
DEFINITION	Homo sapiens chromosome 3 clone 996C6 map 3p, complete sequence.				
ACCESSION	AC022379				
VERSION	AC022379.2	GI:14211546			
KEYWORDS	HTG.				
SOURCE	human				

ORGANISM

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae: Homo.
1 (bases 1 to 223542)
ning v

AUTHORS

Guo, Z., He, L., Hu, S., Huang, F., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., Li, F., Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Li, C., Li, C., Liu, Y., Li, W., Li, W., Li, Y., Luo, C., Luo, J., Niu, Y., Qi, Q., Qi, X., Song, L., Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J., Wang, J., Wang, J., Wang, L., Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y., Wu, D., Wu, Q., Xie, F., Xuan, Z., Xue, Y., Yan, C., Zhang, M., Zhang, X., Zhang, Y., Zhang, G., Zhang, H., Zhang, L., Zhang, L., Zhu, N., Yu, J., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Unpublished

Chromosome 3p genomic sequence

TITLE
JOURNAL

TITLE
JOURNAL

REFERENCE	AUTHORS	TITLE
2 (bases 1 to 222542)	Wan, M., Zhang, C., Dong, H., Lin, W., Xu, S., Gu, W., Tu, Y., Jia, J., Wu, C., Lu, G., Zhong, M., Zhou, Y., Ren, S., Fu, G., Chen, Z. and Huang, M.	Disassembly of the 30S ribosomal subunit of <i>Escherichia coli</i> by a novel method

TITLE
JOURNAL

Submitted (03-FEB-2000) Genomic Dept., Chinese National Human Genome Center at Shanghai, 315 Guo Shou Jing Road, Shanghai, Shanghai 201203, P. R. China
3 (bases 1 to 222542)
n

REFERENCES

Ding, K., Dong, J., Bao, O., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J.,
Ding, H., Ding, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D.,
Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Guo, D.,
Li, F., Li, G., Li, J., Li, S., Li, T., Liu, Y., Liu, N., Li, C., Li, C.,
Liu, Y., Li, W., Li, Y., Luo, C., Luo, J., Liu, Y., Qi, L., Liu, B.,
Song, L., Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Qi, X.,
Wang, J., Wang, J., Wang, L., Wang, L., Wang, R., Wang, H.,
Wang, X., Wang, Y., Wu, D., Wu, Q., Xie, F., Xuan, Z., Wang, X.,
Yang, X., Yu, B., Zeng, Y., Zhang, G., Zhang, H., Zhang, X., Yan, C.,
Zhang, M., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B.,
Zhu, N., Yu, J. and Yang, H.
Direct Submission

ITLE
OURNAL

Received (28-MAY-2001) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100010, P.R.China
On May 28, 2001 this sequence version replaced gi:6862621.
-----Genome Center
Center:Beijing Center
Center code:Beijing
Website:<http://hgci.igtp.ac.cn>
<http://www.genomics.org.cn>
Contact:hgci@igtp.ac.cn

COMMENT

On May 28, 2001 this sequence version replaced gi:6862621.
 Center:Genome Center
 Center:Beijing Center
 Website:http://hgsc.igtp.ac.cn
 http://www.genomics.org.cn
 Contact:hgsc@igtp.ac.cn
 ----- Project Information
 Center project name:1# project
 Center clone name: 996C6

	Project Information
Center project name:	18 project

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Center clone name: 996C6
----- Summary Statistics -----
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator; ET 55% of reads
Assembled: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 226144 bases at least Q40
Consensus quality: 226838 bases at least Q30

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Consensus quality: 226966 bases at least Q20
Insert size: 222542; sum-of-contigs
Quality coverage: 10.14x in Q20 bases;sum-of-contigs

FEATURES
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Location/Qualifiers
1..222542
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p"
/clone="996C6"
57203 a 54087 c 54080 g 57172 t
BASE COUNT
ORIGIN
Query Match 22.5%; Score 35.8; DB 9; Length 222542;
Best Local Similarity 63.2%; Pred. No. 3.3;
Matches 55; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 72 ggcacgagcgatgaataagtggttcacgacctattatccaaaaactgcagaacgtca 131
Db 5160 GACAGGAGCAATAAAAAATCATTTGTTGCAAAAGTGTCCAAAAGTTCACAGAGCTA 5101
QY 132 tacacgcccgcgtatcgatattatta 158
Db 5100 TACATGCCCCAGGCTGTAGGCAACAATTA 5074

RESULT 15
AC006220
LOCUS AC006220 105222 bp DNA PLN 05-APR-2000
DEFINITION Arabidopsis thaliana chromosome II section 28 of 255 of the complete sequence. Sequence from clones F16J10, T20G20, T3P4.
ACCESSION AC006220 AB02093
VERSION AC006220.3 GI:6598532
KEYWORDS HTG
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 105222)
Lin.X., Kaul, S., Rounsley, S.D., Shea, T.P., Benito, M.-I., Town, C.D., Fujii, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E., Feldblyum, T.V., Buell, C.R., Ketchum, K.A., Lee, J.J., Ronning, C.M., Koo, H., Moffat, K.S., Cronin, L.A., Shen, M., VanAken, S.E., Umayam, L., Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H., Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D., Nierman, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and Venter, J.C.
Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
Nature 402 (6763), 761-768 (1999)
20083487
10617197
2 (bases 1 to 105222)
Lin.X.
Direct Submission
Submitted (09-MAR-2000) The Institute for Genomic Research; 9712 Medical Center Dr., Rockville, MD 20850, USA
On Dec 17, 1999 this sequence version replaced gi:4581161.
The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://genomic.stanford.edu/GENSCAN.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST

databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/BM/RepeatMasker.html). Genes are numbered from the top to bottom of the chromosome.

We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13P4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.

This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.

Address all correspondence to: at@tigr.org.
FEATURES
Source
Location/Qualifiers
1..105222
/organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="II"
complement(<1..1080)
/note="Sequence from clone F16J10"
join(<658..774,856..>1305)
/gene="At2g05430"
/gene="At2g05430"
/gene="At2g05430"
/note="F16J10.2; predicted by genefinder"
join(658..774,856..1305)
/gene="At2g05430"
/note="hypothetical protein"
/codon_start=1
/protein_id="AAD24664.2"
/db_xref="GI:6598533"
/translation="MSKISEKSTLSHCHGTAYDELDNDNDEIVNIKGFWRKSLGLAK RVFEKHPETTTKFKLSERAKETILTALDLIDIMNLPQOSLFEALKEAENTLIDL EAAGFKLDWKKRRLKEIRVTKRKRNRTRMRDLRRKHLEELSVLQEMKKRQFE AMCDKPEYLDLSLCLNEVTCDSSEPTK"
complement(1081..105021)
/note="Sequence from clone T20G20"
complement(2070..2185)
/rpt_family="(TAAA)n"
2709..2826
/rpt_family="(TAAA)n"
2750..2864
/rpt_family="(TAA)n"
3314..3367
/rpt_family="(TA)n"
complement(4610..4638)
/rpt_family="POLY-A"
join(<7338..7419,7778..8372,8698..8803,9111..9231,9619..9931)
/gene="At2g05440"
/gene="At2g05440"
/gene="At2g05440"
/note="T20G20.21"
join(7338..7419,7778..8160)
/gene="At2g05440"
/codon_start=1
/product="putative glycine-rich protein"
/protein_id="AAD24663.1"

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2002, 13:48:36 ; Search time 1172.17 Seconds
(without alignments)
1457.620 Million cell updates/sec

Title: US-09-407-804A-8

Perfect score: 159

Sequence: 1 atgttaaccaaagaatttt.....ccgctatcgtcgaattataa 159

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gb_estl1:*
11: gb_estl2:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	36.8	23.1	398	10	AA812069
C 2	36.8	23.1	399	10	AA426563
C 3	36.8	23.1	628	11	BC938678
C 4	36.8	23.1	974	11	BF794164
5	35.6	22.4	704	11	BG169535
6	35.2	22.1	290	11	M86125
7	35.2	22.1	564	13	AQ372904
8	34.2	21.5	277	10	AA684791
C 9	33.4	21.0	328	10	AW903175
C 10	33.4	21.0	346	11	BE812146
11	33.4	21.0	510	10	A1940791
12	33.4	21.0	572	10	A1940804

13	33.4	21.0	659	10	AU137533
C 14	33.2	20.9	856	13	CNS02PPI
15	32.8	20.6	633	13	BH081489
16	32.6	20.5	518	13	AQ251087
17	32.6	20.5	707	13	AZ369151
C 18	32.2	20.3	385	13	AF295591
C 19	32	20.1	225	13	BH6173
C 20	32	20.1	905	13	BH136332
C 21	31.8	20.0	525	13	B65550
C 22	31.8	20.0	721	13	AZ268413
23	31.8	20.0	796	13	BH115293
24	31.6	19.9	910	13	BH136096
C 25	31.6	19.9	849	10	AA896531
C 26	31.6	19.9	859	13	BH136628
C 27	31.4	19.7	525	13	AQ921505
C 28	31.4	19.7	599	13	FR0031459
C 29	31.2	19.6	777	13	CNS0738Y
C 30	31.2	19.6	1102	13	CNS040LM
C 31	31	19.5	625	10	AV745862
C 32	30.8	19.4	465	10	AW515085
C 33	30.8	19.4	662	13	AQ924679
C 34	30.6	19.2	383	10	AL373357
35	30.6	19.2	517	10	AW444057
C 36	30.6	19.2	1101	13	CNS00GIC
C 37	30.4	19.1	246	10	AV273947
C 38	30.4	19.1	755	13	AQ916515
C 39	30.4	19.1	880	13	CNS013QG
40	30.2	19.0	328	10	AI882653
C 41	30.2	19.0	347	10	AA054203
42	30.2	19.0	366	13	AQ247318
43	30.2	19.0	386	11	DB5814
44	30.2	19.0	398	13	AZ640930
45	30.2	19.0	508	10	BE239336

ALIGNMENTS

RESULT 1
AA812069/c
LOCUS
DEFINITION
ob75b07.s1 NCI_CGAP_GCBI Homo sapiens cDNA clone IMAGE:1337173 3' similar to contains element MER22 repetitive element ; , mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
human.
REFERENCE
AUTHORS
TITLE
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2050 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 397.
Location/Qualifiers
1. .398
/organism="Homo sapiens"

```

/db_xref="taxon:9606"
/clone_image="I337173"
/clone_lib="NCI_CGAP_GCBI"
/tissue_type="germinal center B cell"
/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand
cDNA was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGCTCATTTTTCATTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT      136 a      75 c      61 g      125 t      1 others
ORIGIN

Query Match      23.1%; Score 36.8; DB 10; Length 398;
Best Local Similarity 58.0%; Pred. No. 0.88;
Matches 65; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 15 atttttaaaactaaacttggttcagatgttcagctcagaaactcatagatgagc 74
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 347 ATTAAATAAATGTGTATGTGTATATATATACACACATACATATATTATGTC 288

Qy 75 acaggcgatgaaatagggttcagcaccatttatccaaaacttcagaa 126
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 287 ATGTGGTGAAGAATGTGCTAGTAGGGGATTTTCTGAACACTGCAAAAA 236

RESULT 2
AA426003/c      399 bp      mRNA      EST      16-OCT-1997
LOCUS      zw02g04.sl Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:768150
DEFINITION      3', mRNA sequence.
ACCESSION      AA426563
VERSION      AA426563.1 GI:2106818
KEYWORDS      EST
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 399)
AUTHORS      Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie
T., Waterston, R., and Wilson, R.
WashU-Merck EST Project 1997
JOURNAL      Unpublished (1997)
COMMENT      Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -41ml3 fwd. Et from Amersham
High quality sequence stop: 332.
Location/Qualifiers
1..399
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:768150"
/clone_lib="Soares_NHMPU_S1"
/tissue_type="pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"

/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NbHPU, and fetal heart NbH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

BASE COUNT      136 a      77 c      65 g      121 t
ORIGIN

Query Match      23.1%; Score 36.8; DB 10; Length 399;
Best Local Similarity 58.0%; Pred. No. 0.88;
Matches 65; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 15 atttttaaaactaaacttggttcagatgttcagctcagaaactcatagatgagc 74
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 335 ATTAAATAAATGTGTATGTGTATATATATACACACATACATATATTATGTC 276

Qy 75 acaggcgatgaaatagggttcagcaccatttatccaaaacttcagaa 126
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275 ATGTGGTGAAGAATGTGCTAGTAGGGGATTTTCTGAACACTGCAAAAA 224

RESULT 3
BG938678/c      628 bp      mRNA      EST      11-JUN-2001
LOCUS      cn27f10.xl Normal Human Trabecular Bone Cells Homo sapiens cDNA
DEFINITION      clone NHTBC_cn27f10 random, mRNA sequence.
ACCESSION      BG938678
VERSION      BG938678.1 GI:14338050
KEYWORDS      EST
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 628)
AUTHORS      Jia, L.B., Young, M.F., Touchman, J.W., Bouffard, G.G.,
Beckstrom-Sternberg, S.M., Green, E.D., Powell, J.I., Yang, L.M., Robey
P.G., Hotchkiss, R.N. and Francomano, C.A.
SCAP: The Skeletal Genome Anatomy Project
Unpublished (1997)
JOURNAL      Contact: Libin Jia
COMMENT      Medical Genetics Branch
National Human Genome Research Institute
10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
Tel: 301-402-4877
Fax: 301-496-7157
Email: libin@helix.nih.gov
DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).
Plate: 27 row: f column: 10
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
1..628
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NHTBC_cn27f10"
/clone_lib="Normal Human Trabecular Bone Cells"
/sex="Female"
/tissue_type="Bone"
/cell_type="Trabecular Bone Cells"
/lab_host="SURE"
/note="Organ: Hip; Vector: pBluescript; Site_1: EcoRI"

BASE COUNT      183 a      149 c      117 g      179 t
ORIGIN

Query Match      23.1%; Score 36.8; DB 11; Length 628;

```


The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlavetigr.org

Seq primer: M13 Forward.
Location/Qualifiers
1..290

FEATURES

source

/organism="Homo sapiens"
/db_xref="ATCC (inhost):81702"
/db_xref="GDB:D05813E"
/db_xref="taxon:9606"
/clone="HFEUDJ72"
/note="Vector: Fetal brain, Stratagene (cat#936206)"
oligo-dt + random primed cDNA synthesis; LambdaZAP-II
vector, 1.0kb average inser size."

BASE COUNT 86 a 34 c 67 g 102 t 1 others
ORIGIN

Query Match 22.1%; Score 35.2; DB 11; Length 290;
Best Local Similarity 57.1%; Pred. No. 2.5;
Matches 64; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
Qy 15 atttttaaaactaaactgagtttcagatgtacgtctcagaactcatagatgagc 74
Db 156 ATTTAAATAAATGTGTGTGTGTATATATATATACACACATACATATATTATGC 215
Qy 75 acagggcgatgaatgagttgtcagcacttatttccaaacactcgagaa 126
Db 216 ATGTGGTGAAGAAGATTGGCTAGATAGGGGATTTTCTTCACACTGCAAAA 267

RESULT

7

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Other_GSSs: RPC11-158H17.TV

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbeetigr.org

Clones are derived from the human BAC library RPC1-11. For BAC

library availability, please contact Pietr de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (http://resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Seq primer: S56

Class: BAC ends.

Location/Qualifiers

1..564

/organism="Homo sapiens"

/db_xref="GDB:7560472"

/db_xref="taxon:9606"

FEATURES

source

1..564

/organism="Homo sapiens"

/db_xref="GDB:7560472"

/db_xref="taxon:9606"

/clone="RPC1-11-158H17"

/clone_lib="RPC1-11"

/sex="Male"

/cell_type="Lymphocytes"

/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC111 Human Male BAC Library"

BASE COUNT 169 a 110 c 147 g 138 t

ORIGIN

Query Match 22.1%; Score 35.2; DB 13; Length 564;

Best Local Similarity 58.7%; Pred. No. 2.7;

Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 14 aatttttaaaactaaactgagtttcagatgtacgtctcagaactcatagatgagc 73

Db 328 AATTGTGTAACAGAAATGACCTGATCAGATTGTGTTTAAAGGTATAGACTTGA 387

Qy 74 cacagggcgatgaatgagttgtcagcacttatttccaaaaa 117

Db 388 ATCAGGCAGACCAATTAACTGAGATGCCACAAATTATCCAAACA 431

RESULT 8

AA684791

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

Other_ESTs: EST105418

Contact: Lee, NH

The Institute for Genomic Research

9712, Medical Center Drive, Rockville, MD 20850, USA

Tel: (301)-838-3529

Fax: (301)-838-0208

Email: nhlee@tigr.org

Seq primer: M13 Reverse.

Location/Qualifiers

1..277

/organism="Rattus sp."

/db_xref="ATCC (inhost):2000525"

/db_xref="taxon:10118"

/clone="RPCAJ06"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

XhoI; poly(A)+ RNA was purified from untreated PC12 cells

cultured for 9 days. cDNA was constructed using an

oligo-dt primer and directionally cloned using the Lambda

ZAP II Vector kit by Stratagene"

BASE COUNT 95 a 46 c 62 g 72 t

ORIGIN

Query Match 21.5%; Score 34.2; DB 10; Length 277;

Best Local Similarity 53.9%; Pred. No. 4.9;

Matches 69; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

RESULT 11
 AI940791
 LOCUS CM0-ST0050-220799-029-f05 ST0050 Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 ACCESSION AI940791 EST 03-AUG-1999
 VERSION
 KEYWORDS AI940791.1 GI:5687772
 SOURCE EST.
 ORGANISM human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 510)
 HCCP <http://www.ludwig.org.br/ORESTES>
 The FAPESP/LICR Human Cancer Genome Project
 Unpublished (1999)
 CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM0&t2=CM0-ST0050-220799-029-f05&t3=1999-07-22&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 85
 High quality sequence stop: 504.
 FEATURES
 Location/Qualifiers
 1..510
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="ST0050"
 /dev_stage="Adult"
 /note="Organ: Stomach; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 164 a 98 c 132 g 116 t

BASE COUNT
 ORIGIN

Query Match 21.0%; Score 33.4; DB 10; Length 510;
 Best Local Similarity 62.7%; Pred. No. 9.1;
 Matches 52; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
 QY 57 gaaactcatagatgagccacagcgcatgaaataggtgtacgacctattatccaaaa 116
 Db 66 GAGACTCTTGATGATACACGGGAGCAGAAAGGTGCTGCACTATCTGGCAATCCAGAA 125
 QY 117 acttcagaaagctatcacagcc 139
 Db 126 ACCTGCAGACCTTGTCTCGGCACC 148

RESULT 12
 AI940804
 LOCUS CM0-ST0050-260799-031-f05 ST0050 Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 ACCESSION AI940804 EST 03-AUG-1999
 VERSION
 KEYWORDS AI940804.1 GI:5687785
 SOURCE EST.
 ORGANISM human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 572)
 HCCP <http://www.ludwig.org.br/ORESTES>
 The FAPESP/LICR Human Cancer Genome Project
 Unpublished (1999)
 CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

AUTHORS
 TITLE
 JOURNAL
 COMMENT

HCCP <http://www.ludwig.org.br/ORESTES>
 The FAPESP/LICR Human Cancer Genome Project
 Unpublished (1999)
 CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM0&t2=CM0-ST0050-260799-031-f05&t3=1999-07-26&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 28
 High quality sequence stop: 571.
 FEATURES
 Location/Qualifiers
 1..572
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="ST0050"
 /dev_stage="Adult"
 /note="Organ: stomach; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 187 a 107 c 152 g 126 t

BASE COUNT
 ORIGIN

Query Match 21.0%; Score 33.4; DB 10; Length 572;
 Best Local Similarity 62.7%; Pred. No. 9.2;
 Matches 52; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
 QY 57 gaaactcatagatgagccacagcgcatgaaataggtgtacgacctattatccaaaa 116
 Db 131 GAGACTCTTGATGATACACGGGAGCAGAAAGGTGCTGCACTATCTGGCAATCCAGAA 190
 QY 117 acttcagaaagctatcacagcc 139
 Db 191 ACCTGCAGACCTTGTCTCGGCACC 213

RESULT 13
 AI137533
 LOCUS AU137533 PLACE1 Homo sapiens cDNA clone PLAC1006685 5', mRNA
 DEFINITION
 ACCESSION AU137533
 VERSION AU137533.1 GI:10998072
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 659)
 Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
 Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
 Isogai,T.
 HRI human cDNA project
 Unpublished (2000)
 CONTACT: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yano, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3951
 Fax: 81-438-52-3952
 Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES

source Location/Qualifiers

1..859
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1006685"
/clone_lib="PLACE1"
/tissue_type="placenta"
/note="Vector: pME18SFL3"

208 a 126 c 171 g 151 t 3 others

BASE COUNT

ORIGIN

Query Match 21.0%; Score 33.4; DB 10; Length 659;
Best Local Similarity 62.7%; Pred. No. 9.3;
Matches 52; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 gaaactcatagatgagccagggcagatgaaataggtgtgacgacctattatccaaa 116

DB 284 GAGACTCTTCGATACATACAGGAGCAGCAAGAGGTGCTGCACATCTCGCAATCCAGAA 343

QY 117 acttgcagaacgtcatcacgc 139

DB 344 ACCTGCAGACCTTGCTCGGCACC 366

RESULT 14

CNS02PPI/c

LOCUS

DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 156A20 of library G from Tetraodon nigroviridis, genomic survey

sequence.

AL208287

QY 117 856 bp DNA GSS 14-MAY-2000

VERSION GSS: genome survey sequence.

KEYWORDS Tetraodon nigroviridis.

SOURCE Tetraodon nigroviridis.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Tetraodon.

1 (bases 1 to 856)

Roest-Crolius, H., Jaillon, O., Dasilva, C., Fizes, C., Fisher, C.,

Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and

Weissenbach, J.

Characterization and repeat analysis of the compact genome of the

freshwater pufferfish Tetraodon nigroviridis

Unpublished

2 (bases 1 to 856)

Roest-Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,

Bernot, A., Fizes, C., Wincker, P., Brottier, P., Quetier, F.,

Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using

Tetraodon nigroviridis DNA sequence

Unpublished

3 (bases 1 to 856)

Roest-Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,

Bernot, A., Fizes, C., Wincker, P., Brottier, P., Quetier, F.,

Saurin, W. and Weissenbach, J.

Genoscope.

Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

This sequence is a single read and was generated as part of a large

scale clone-end sequencing project of the Tetraodon nigroviridis

genome. For more information, please take a look at

http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers

1..856

/organism="Tetraodon nigroviridis"

/db_xref="taxon:99883"

/clone="156A20"

/clone_lib="G"

/note="Genoscope sequence ID : COAG156BA10LPI-end : T7"

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches 71; Conservative

1; Mismatches

64; Indels

0; Gaps

0;

QY 19 ttaaaactaaacttgagttcagatagtacgtcagaaactcatagatgagggcag 78

DB 264 TTAATAATATATAGAAATATATATCAATCCATTCAGTAATGATATATTATTAACAG 205

QY 79 ggcgatgaaaataggtgtgacgacctattatccaaaacttgcagaacgtcatcacgc 138

DB 204 GAAAGGAAAGAGGCTGAAACACACACCCCTTTTCATAAACTTCTAGTTGGSCCCCT 145

QY 139 cccgctatcgtcgaat 154

DB 144 CCTTCTGCCCTAATAT 129

RESULT 15

BH081489

LOCUS

DEFINITION

BH081489

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 633)

Zhao, S., Nierman, W., Malek, J., Shatsman, S., Aklnret, B., Levins, M.,

Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,

Russell, D., de Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-24

Unpublished (1999)

Other_GSSs: RPCI-24-321117.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC

library availability, please contact Pieter de Jong

(pdejong@mail.cho.org). Clones may be purchased from BACPAC

Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end

page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 321 row: 1 column: 17

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..633

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-321117"

/clone_lib="RPCI-24"

/sex="Male"

/cell_type="Spleen/Brain"

/note="Vector: pTABAC1; site_1: BamHI; site_2: BamHI;

RPCI-24 Mouse BAC Library produced by Pieter de Jong. The

library was cloned in the pTABAC1 cloning vector at the

BamHI sites using MboI partially digested male C57BL/6J

DNA."

190 a 93 c 171 g 179 t

BASE COUNT

ORIGIN

us-09-407-804a-8.rst

Page 8

	Query Match	20.6%	Score 32.8;	DB 13;	Length 633;
	Best Local Similarity	61.9%	Pred. No. 14;		
	Matches 52;	Conservative 0;	Mismatches 32;	Indels 0;	Gaps 0;
QY	56	agaaactcatgatgagcgacagggcgatgaaatagggtgtacacacctattatccaaa			
Db	257	AGAGACTCATAGGTCAGCTACAGGGATTGTGTAAGCTATTAGTAGAGTTTCCAAT			
QY	116	aacttgcgaacggtcatcacgcgc			
Db	317	GACTTGTGTCACACATTCATCCC			

Search completed: March 1, 2002, 14:32:19
Job time: 2623 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2002, 13:48:36 ; Search time 38.97 seconds
(without alignments)
924.044 Million cell updates/sec

Title: US-09-407-804A-8
Perfect score: 159
Sequence: 1 atgttaacacaaagaatttt.....ccgctatcgtcgatattaa 159

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues
Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	29.4	18.5	491	4	US-09-189-060B-17
C 2	28.8	18.1	394	1	US-08-650-275-12
C 3	28.8	18.1	394	3	US-09-181-318-12
C 4	28.6	18.0	3012	1	US-07-991-867B-21
C 5	28.6	18.0	3012	1	US-08-107-755A-21
C 6	28.6	18.0	3012	2	US-08-544-332-21
C 7	28.6	18.0	3907	1	US-07-991-867B-33
C 8	28.6	18.0	3907	1	US-08-107-755A-33
C 9	28.6	18.0	3907	2	US-08-544-332-33
C 10	28.6	18.0	6768	1	US-08-107-755A-1
C 11	28.6	18.0	8457	1	US-07-991-867B-1
C 12	28.6	18.0	8457	2	US-08-544-332-1
C 13	28.2	17.7	5340	3	US-08-492-459-9
C 14	28.2	17.7	5340	3	US-08-423-752-9
C 15	28.2	17.7	5340	3	US-08-945-994-2
C 16	28.2	17.7	5340	4	US-08-716-873-23
C 17	28.2	17.7	5340	4	US-09-368-431-23
C 18	27.6	17.4	1811	2	US-08-808-931-9
C 19	27.6	17.4	1811	3	US-08-808-323-9
C 20	27.6	17.4	1811	3	US-09-050-603A-9
C 21	27.6	17.4	1811	3	US-09-102-420B-9
C 22	27.4	17.2	4766	5	PCT-US93-07261-10
C 23	27.2	17.1	656	4	US-09-328-111-313
C 24	27.2	17.1	9751	4	US-09-238-303-7
C 25	27	17.0	2293	1	US-08-604-913B-12
C 26	27	17.0	3004	1	US-08-276-213-6
C 27	27	17.0	4322	1	US-08-673-789-1

C 28	26.8	16.9	20137	4	US-09-262-773-206
C 29	26.8	16.9	20138	4	US-09-262-773-9
C 30	26.8	16.9	23071	4	US-09-262-773-210
C 31	26.6	16.7	771	4	US-08-998-416-474
C 32	26.6	16.7	1090	6	5223424-1
C 33	26.6	16.7	1392	3	US-08-989-510A-10
C 34	26.6	16.7	1392	3	US-08-989-510A-11
C 35	26.6	16.7	1392	3	US-09-182-816-10
C 36	26.6	16.7	1392	3	US-09-182-816-12
C 37	26.6	16.7	1392	3	US-09-471-528-10
C 38	26.6	16.7	1392	3	US-09-471-528-12
C 39	26.6	16.7	1392	4	US-09-634-530-10
C 40	26.6	16.7	1392	4	US-09-634-530-12
C 41	26.6	16.7	1605	3	US-08-989-510A-7
C 42	26.6	16.7	1605	3	US-08-989-510A-9
C 43	26.6	16.7	1605	3	US-09-182-816-7
C 44	26.6	16.7	1605	3	US-09-182-816-9
C 45	26.6	16.7	1605	3	US-09-471-528-7

ALIGNMENTS

RESULT 1
US-09-189-060B-17/c
; Sequence 17, Application US/09189060B
; Patent No. 6270968
; GENERAL INFORMATION:
; APPLICANT: Dalboge, Henrik
; APPLICANT: Sandal, Thomas
; APPLICANT: Kauppinen, Markus
; APPLICANT: Borge, Diderichsen
; TITLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences
; FILE REFERENCE: 4772.204-US
; CURRENT APPLICATION NUMBER: US/09/189,060B
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/DK97/00216
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Hybrid
US-09-189-060B-17

Query Match 18.5%; Score 29.4; DB 4; Length 491;
Best Local Similarity 64.6%; Pred. No. 0.43;
Matches 42; Conservative 1; Mismatches 22; Indels 0; Gaps 0;

Qy 92 gttgtacagacctatttccaaaacttgcagaacgtcatcacgcccgcgtatcgtcg 151
|||:| | ||||| | ||| | | ||| | | ||||| | | | | |
Db 238 GGTGTGTCCTACCTATCAGTACAGGACAGAACACCAAGAACTCGCTGTGGCTG 179
Qy 152 aatat 156
|||:| | ||||| |
Db 178 AATAT 174

RESULT 2
US-08-650-275-12/c
; Sequence 12, Application US/08650275
; Patent No. 5798249
; GENERAL INFORMATION:
; APPLICANT: Braxton, Scott Michael
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN PROTEIN DISULFIDE ISOMERASE
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto

STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650.275
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0067 US
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY: LVENNOT01
CLONE: 350290
US-08-650-275-12

Query Match 18.1%; Score 28.8; DB 1; Length 394;
Best Local Similarity 63.9%; Pred. No. 0.63;
Matches 39; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
Qy 72 ggcacagggcgatgaataagggtgtacgacctattatcccaaaacttcgagaacgtca 131
Db 384 GNCAAACGGNATGTAAGGTTATTGGACCTTTTCNCCTATTATTATTCGCCGAGCTTCN 325
Qy 132 t 132
Db 324 T 324

RESULT 3
US-09-181-318-12/c
Sequence 12, Application US/09181318
Patent No. 6001632
GENERAL INFORMATION:
APPLICANT: Braxton, Scott Michael
APPLICANT: Murty, Lynn E.
TITLE OF INVENTION: HUMAN PROTEIN DISULFIDE ISOMERASE
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/181.318
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/650.275
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.

REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0067 US
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY: LVENNOT01
CLONE: 350290
US-09-181-318-12

Query Match 18.1%; Score 28.8; DB 3; Length 394;
Best Local Similarity 63.9%; Pred. No. 0.63;
Matches 39; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
Qy 72 ggcacagggcgatgaataagggtgtacgacctattatcccaaaacttcgagaacgtca 131
Db 384 GNCAAACGGNATGTAAGGTTATTGGACCTTTTCNCCTATTATTATTCGCCGAGCTTCN 325
Qy 132 t 132
Db 324 T 324

RESULT 4
US-07-991-867B-21
Sequence 21, Application US/07991867B
Patent No. 5476781
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991.867B
FILING DATE: 12-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827.685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657.584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: Uf114.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800

; MOLECULE TYPE: DNA (genomic)

Db 1917 TTACAAATTAATAAATTTATGTAGATACGACGAAATAAAATTTATATTGGAAGAAA 1976
QY 77 agggcgatgaatagtgtagacacatttaccgaaacttgacgaacgtcatcac 136
Db 1977 TTGAAGCAGAATATAGATCGGAGACAGTATTCCACGACGTTGTAATAAAC 2036
QY 137 gcc 139
Db 2037 ACC 2039

RESULT 9
US-08-544-332-33
; Sequence 33, Application US/08544332
; Patent No. 5935777
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Hall, Richard L.
; APPLICANT: Gruidl, Michael E.
; TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gerard H. Bencen
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/544,332
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,867
; FILING DATE: 07-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/107,755
; FILING DATE: 19-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 92/14818
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,685
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/657,584
; FILING DATE: 19-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bencen, Gerard H.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: UF114.C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3907 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; US-08-544-332-33

Query Match 18.0%; Score 28.6; DB 2; Length 3907;
Best Local Similarity 52.0%; Pred. No. 1.7;
Matches 64; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 17 ttttaaaactaaacttgagtgttcagatatgtacgtccgaaaactcatagatgagggcac 76
Db 1917 TTTACAAATTAATAAATTTATGTAGATACGACGAAATAAAATTTATATTGGAAGAAA 1976
QY 77 agggcgatgaatagtgtagacacatttaccgaaacttgacgaacgtcatcac 136
Db 1977 TTGAAGCAGAATATAGATCGGAGACAGTATTCCACGACGTTGTAATAAAC 2036
QY 137 gcc 139
Db 2037 ACC 2039
RESULT 10
US-08-107-755A-1
; Sequence 1, Application US/08107755A
; Patent No. 5721352
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Hall, Richard L.
; APPLICANT: Gruidl, Michael E.
; TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: U.S.A.
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,755A
; FILING DATE: 19-AUG-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,658
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/657,584
; FILING DATE: 19-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF114.C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ORGANISM: Amsacta moorei entomopoxvirus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (65..1459)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1474..2151
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (2239..2475)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2502..2987

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;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3080...6091
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (6277..6768)
;
US-08-107-755A-1

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Query Match      18.0%; Score 28.6; DB 1; Length 6768;
Best Local Similarity 52.0%; Pred. No. 2.1;
Matches 64; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 17 ttttaaaactaaacttgagttgcagatgtacgctcagaactcatagatgagggcac 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4191 TTTACAAATTAATAAATTTATGTAGATAACGACGAAATATAATTTGGAAGAAA 4250
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 77 agggcgatgaaatagggtgtacgacctattatccaaaacttcgagaacgtcatcac 136
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4251 TTGAAGCAGATATAGATGCCGAAGACAAGTATTCACGAACGTGTAATAAAC 4310
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 137 gcc 139
    ||
Db 4311 ACC 4313
    ||

```

```

RESULT 11
US-07-991-867B-1
; Sequence 1, Application US/07991867B
; Patent No. 5476781
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Hall, Richard L.
; APPLICANT: Gruidl, Michael E.
; TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/991.867B
; FILING DATE: 12-DEC-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 92/14818
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,685
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/657,584
; FILING DATE: 19-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF114.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8457 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
;

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;
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Amsacta moorei entomopoxvirus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (65..1459)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1474..2151
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (2239..2475)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2502..2987
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3080..6091
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (6277..6768)
;
US-07-991-867B-1

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Query Match      18.0%; Score 28.6; DB 1; Length 8457;
Best Local Similarity 52.0%; Pred. No. 2.2;
Matches 64; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 17 ttttaaaactaaacttgagttgcagatgtacgctcagaactcatagatgagggcac 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4191 TTTACAAATTAATAAATTTATGTAGATAACGACGAAATATAATTTGGAAGAAA 4250
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 77 agggcgatgaaatagggtgtacgacctattatccaaaacttcgagaacgtcatcac 136
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4251 TTGAAGCAGATATAGATGCCGAAGACAAGTATTCACGAACGTGTAATAAAC 4310
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 137 gcc 139
    ||
Db 4311 ACC 4313
    ||

```

```

RESULT 12
US-08-544-332-1
; Sequence 1, Application US/08544332
; Patent No. 5935777
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Hall, Richard L.
; APPLICANT: Gruidl, Michael E.
; TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gerard H. Bencen
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/544,332
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,867
; FILING DATE: 07-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/107,755

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;; FILING DATE: 19-AUG-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO 92/14818
;; FILING DATE: 12-FEB-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/827,685
;; FILING DATE: 30-JAN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/657,584
;; FILING DATE: 19-FEB-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bencen, Gerard H.
;; REGISTRATION NUMBER: 35,746
;; REFERENCE/DOCKET NUMBER: UF114.C4
;; TELEPHONE: 904-375-8100
;; TELEFAX: 904-372-5800
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8457 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: unknown
;; MOLECULE TYPE: DNA (genomic)
;; ORIGINAL SOURCE:
;; ORGANISM: Anaseta moorei entomopoxvirus
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: complement (65..1459)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1474..2151
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: complement (2239..2475)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 2502..2987
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 3080..6091
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: complement (6277..6768)
US-08-544-332-1

Query Match 18.0%; Score 28.6; DB 2; Length 8457;
Best Local Similarity 52.0%; Pred. No. 2.2;
Matches 64; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 17 ttttaaaactaaacttggtgttcagatatgtacgctcagaaactcatagtgaggcac 76
DB 4191 TTTACAAATTAATAAATAATTTATGTAGATAACGACGAAATAAATATATTGGAGAAA 4250
QY 77 agggcgatgaaatagggtgttcagacctatttaccaaaacttcagaaactcatatcac 136
DB 4251 TTGAAGCAGAATATAGATGCGGAAGACAGATATTCACGAACGTGTAAACCTTAATAAAC 4310
QY 137 gcc 139
DB 4311 ACC 4313

RESULT 13
US-08-492-459-9
; Sequence 9, Application US/08492459
; Patent No. 6015689
; GENERAL INFORMATION:
; APPLICANT: Takashi OKADO et al.
; TITLE OF INVENTION: REGULATION OF AUREOBASIDIN SENSITIVITY IN FUNGUS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Wenderoth, Lind & Ponack
;; STREET: 805 Fifteenth Street, N.W., #700
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 mb
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: Wordperfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/492,459
;; FILING DATE: June 20, 1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/243,403
;; FILING DATE: May 16, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek, Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX:
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5340
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: genomic DNA
US-08-492-459-9

Query Match 17.7%; Score 28.2; DB 3; Length 5340;
Best Local Similarity 54.3%; Pred. No. 2.6;
Matches 57; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 13 gaatttttaaaactaaacttggtgttcagatatgtacgctcagaaactcatagtgag 72
DB 753 GATATTTTCCCTCAGAAACGTGTGTTTTCATTCTTGCACCTCTAAGAAATTCAGAGA 812
QY 73 gcacaggcgatgaaatagggtgttcagacctatttaccaaaa 117
DB 813 CCACAACCGATGACGAGAGAGATATATCTCTCTCCATACA 857

RESULT 14
US-08-423-752-9
; Sequence 9, Application US/08423752
; Patent No. 6022949
; GENERAL INFORMATION:
; APPLICANT: Takashi OKADO et al.
; TITLE OF INVENTION: A GENE CODING FOR A PROTEIN REGULATING
; TITLE OF INVENTION: AUREOBASIDIN SENSITIVITY
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/423,752
; FILING DATE: April 18, 1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/243,403
FILING DATE: May 16, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5340
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-423-752-9

Query Match 17.7%; Score 28.2; DB 3; Length 5340;
Best Local Similarity 54.3%; Pred. No. 2.6;
Matches 57; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 13 gaatttttaaaactgaacttgagtggttcagatatgtacgctcagaaactcatagatgag 72
Db 753 GATATTTCCCTCAGAAACGTCGTTTTCATCTTGCACTCTAAGAAATTCAGAAGTA 812
QY 73 gcacagggcgatgaaataggtgttacgacctattttatccaaaa 117
Db 813 CCACAACCGATGACGAGAGGAGATATATCTCTCTTCCATACA 857

RESULT 15
US-08-945-994-2
Sequence 2, Application US/08945994
Patent No. 6043051
GENERAL INFORMATION:
APPLICANT: Takashi OKADO et al.
TITLE OF INVENTION: PROMOTER
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,994
FILING DATE: No. 6043051ember 6, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5340

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-945-994-2

Query Match 17.7%; Score 28.2; DB 3; Length 5340;
Best Local Similarity 54.3%; Pred. No. 2.6;
Matches 57; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 13 gaatttttaaaactgaacttgagtggttcagatatgtacgctcagaaactcatagatgag 72
Db 753 GATATTTCCCTCAGAAACGTCGTTTTCATCTTGCACTCTAAGAAATTCAGAAGTA 812
QY 73 gcacagggcgatgaaataggtgttacgacctattttatccaaaa 117
Db 813 CCACAACCGATGACGAGAGGAGATATATCTCTCTTCCATACA 857

Search completed: March 1, 2002, 13:49:41
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